

Figure 1

	10	20	30	40	50
XYN2_TRIRE	---	MVSFTSLLAASPP-SRASC	RPAAEV---	ESVAVEKRQTIQ----	P
XYN1_HUMIN	---	MVSLKSVLAAATAVSSAIAAP	FDVPRDNSTALQARQVTP----	N	
XYNA_BACST	-----	-----	MKLKKKMLTLLLTASMSFGLF----	G	
XYN1_TRIRE	---	MVAFSSLICALTSTIASTLAMPT	GLEPESSVNVTERGMYDFVLGAHND		
XYN1_ASPAW	-----	-----	MKVTAAFAGLLVTAFAPVPEPVLVS----		
XYN2_BACST	MCSSIPSLREVFANDFRIGA	AVNPVTLEAQQSLLIRHVNSLTAENHMKFE			

	60	70	80	90	100
XYN2_TRIRE	GTGYNNGYFY	SYWNDGHGGV	TYTNGPGGQFSVNWS--	NSG-NFVGKGKQWQ	
XYN1_HUMIN	AEGWHNGYFY	SWWSDGGGQVQYTNLEGSRYQVRWR--	NTG-NFVGKGKWN		
XYNA_BACST	ATSSAATDYWQY	WTDGGGMVNAVNGPGGNYSVTWQ--	NTG-NFVGKGKWT		
XYN1_TRIRE	HRRRASINYDQNY	QTG-GQVSYSPSNTG-FSVNWN--	TQD-DFVVGVGWT		
XYN1_ASPAW	--RSAGINYVQNY	NGNLGDFTYDESAGT-FSMYWEDGVSS-DFVVGGLGWT			
XYN2_BACST	HLQPEEGRFTFDIAIKS	STSPFSSHGVRGHTLVWHNQTPSWVPQDSQGHF			

	110	120	130	140	150
XYN2_TRIRE	PGTKNKVINFS-GSYNPNGNSYLSVYGWSRNPLIEYYIVENF--	GTYNP			
XYN1_HUMIN	PGT-GRITINYG-GYFNPQNGYLAVYGWTRNPLVEYYVIESY--	GTYNP			
XYNA_BACST	VGSPNRVINYNAGIWEPSGNGYLTLYGWTRNALIEYYVVDW--	GTYP			
XYN1_TRIRE	TGS-SAPINFGGSFSVNSGTGLLSVYGWSTNPLVEYYIMED----	NHNY			
XYN1_ASPAW	TGS-SNAITYSAEYSASGSSSYLAVYGWVNYPPQAEYYIVEDY--	GDYNP			
XYN2_BACST	VGRDVLLERMKSHISTVVQRYKGKVYCWDVINEA VADEGSEWLRSSTWRQ				

	160	170	180	190	200
XYN2_TRIRE	STGATKLGEVTS	SDGSVYDIYRTQ	RVNQPSII	GTATFYQYWSVRRNHRSSG	
XYN1_HUMIN	GSQAQYKGTFTY	TDGDQYDIFVSTRYNQPSIDG	TRTFQYQYWSIRKNKRVGG		
XYNA_BACST	T--GNYKGTVNSDGGTY	DIYTTMRYNAPSIDGTQTFQQFWSVRQSKRPTG			
XYN1_TRIRE	PAQGTVKGTVTS	DGATYTIWENTRVNEPSIQGTATFNQYISVRNSPRTSG			
XYN1_ASPAW	CSSATSLGT	VYSDGSTYQVCTDTRTNEPSITGTSTFTQYFSVRESTRTSG			
XYN2_BACST	IIGDDFIQQAFLYAHEADPEALLFYNDYNECFPEKREKIYTLVKSLRDKG				

Figure 1

	210	220	230	240	250
XYN2_TRIRE	S----	VNTANHFNAWA-QQGLTLGTMD-YQIVAVEGYFSSGSASITVS--			
XYN1_HUMIN	S----	VNMQNHFNAWQ-QHGMPLGQHY-YQVVATEGYQSSGESDIYVQTH			
XYNA_BACST	SNV-SITFSNHVNAWR-SKGMNLGSSWAYQVLATEGYQSSGRSNVTW--				
XYN1_TRIRE	T----	VTVQNHFNAWA-SLGLHLGQMN-YQVVAVEGWGGSGSASQSVSN-			
XYN1_ASPAW	T----	VTVANHFNFWA-QHGFNGSDFN-YQVMAVEAWSGAGSASVTISS-			
XYN2_BACST	IPIHGIGMQAHWSLNRPTLDEIRAAIERYASLGVILHITELDISMFEFDD				

	260	270	280	290	300
XYN2_TRIRE	-----	-----	-----	-----	-----

Figure 1

XYN1_HUMIN	-----
XYNA_BACST	-----
XYN1_TRIRE	-----
XYN1_ASPAW	-----
XYN2_BACST	HRKDLAAPTNE MVERQAERYEQIFSLFKEYRDVIONVTFWGIADDHTWLD

	310	320	330
XYN2_TRIRE	-----		
XYN1_HUMIN	-----		
XYNA_BACST	-----		
XYN1_TRIRE	-----		
XYN1_ASPAW	-----		
XYN2_BACST	HFPVQGRKNWPLL	FDEQHNP	KPAFWRVVNI

FIGURE 2

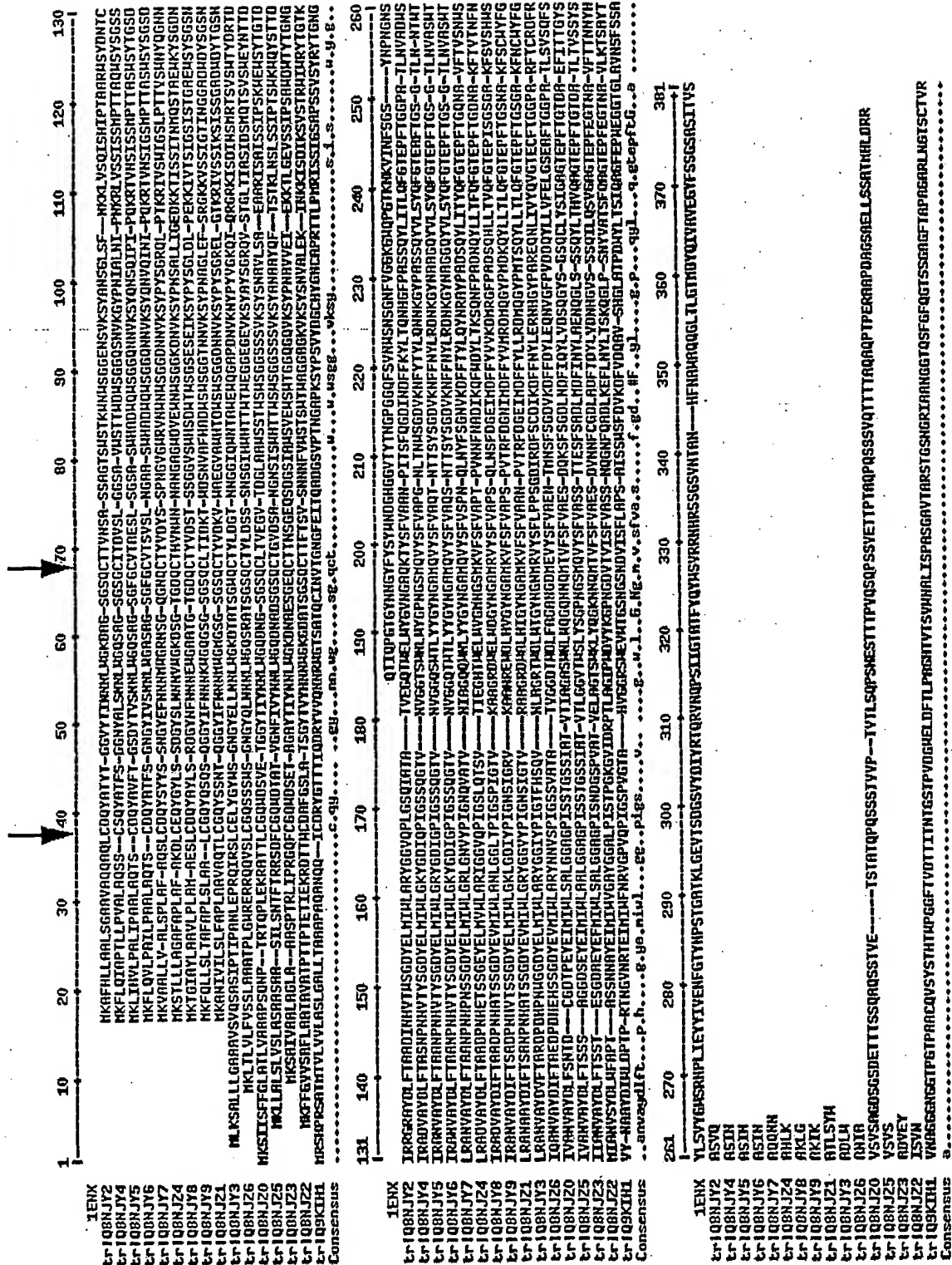


Figure 3

H22K	5'- GAACGATGGCAAGGGCGGCGTGACG -3'
S65C	5'- CTTCTCGGGCTGCTACAACCCAAACGG -3'
N92C	5'- ACATCGTCGAGTGTTTTGGCACCTAC -3'
F93W	5'- CATCGTCGAGAACTGGGGCACCTACAACC -3'
N97R	5'- GGCACCTACCGACCGTCCACG -3'
V108H	5'- CAAGCTGGGCGAGCACACCTCCGAC -3'
H144C	5'- CGCCGCAACTGTCGCTCGAGC -3'
F180Q	5'- GTGGAGGGTTACCAAAGCTCTGGCTCTGC -3'
S186C	5'- TCTGGCTCTGCTTGCATACCGTCAGC -3'
T2C	5'-GAGAAGCGCCAGTGCATTAGCCCGGC-3'
T28C	5'-GTGACGTACTGCAATGGTCCCGGCGGG-3'
K58R	5'-GGCACCAAGAACAGGGTCATCAACTTCTCGGGC-3'
191D	5'-TCCATCACCGTCAGCGATTAAAGGGGGCTCTTC-3'
P5C	5'-CCCAGACGATTAGTGCGGCACGGGCTACAAC-3'
N19C	5'-CTTCTACTCGTACTGGTGCGATGGCCACGGCG-3'
T7C	5'-CGATTAGCCCGGCTGCGGCTACAACAACGGC-3'
S16C	5'-CAACGGCTACTTCTACTGCTACTGGAACGATGGCC-3'
N10C	5'-CCGGCACGGGCTACTGCAACGGCTACTTCTACTC-3'
N29C	5'-GGCGTGACGTACACCTGCGGTCCCGGCGGGC-3'
L105C	5'-GGCGCCACCAAGTGCGGCGAGGTCACC-3'
Q162C	5'-GCGTGGGCTCAGTGCGGCCTGACGCTCG-3'

Figure 4.

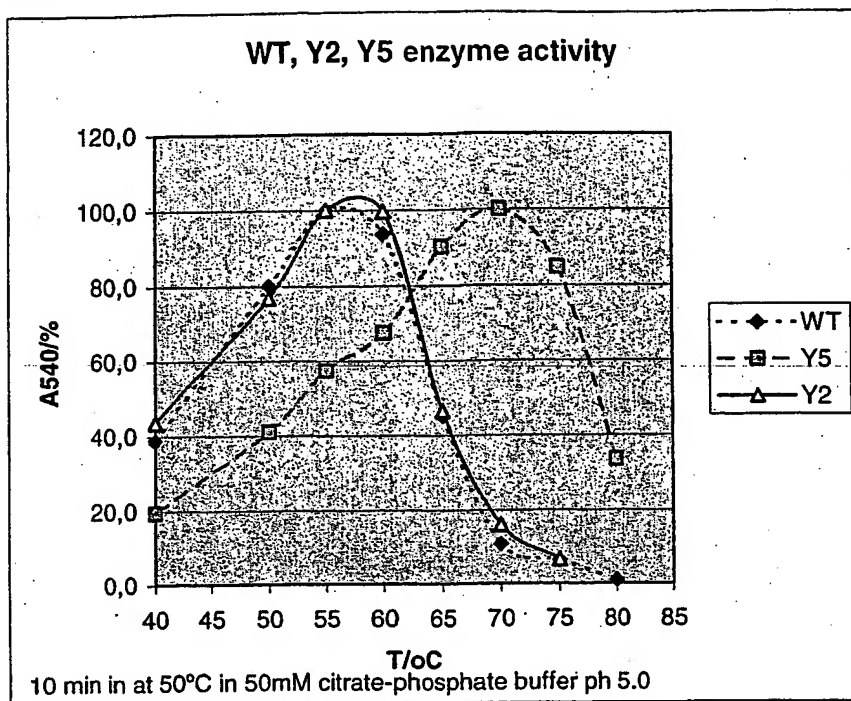


Figure 5

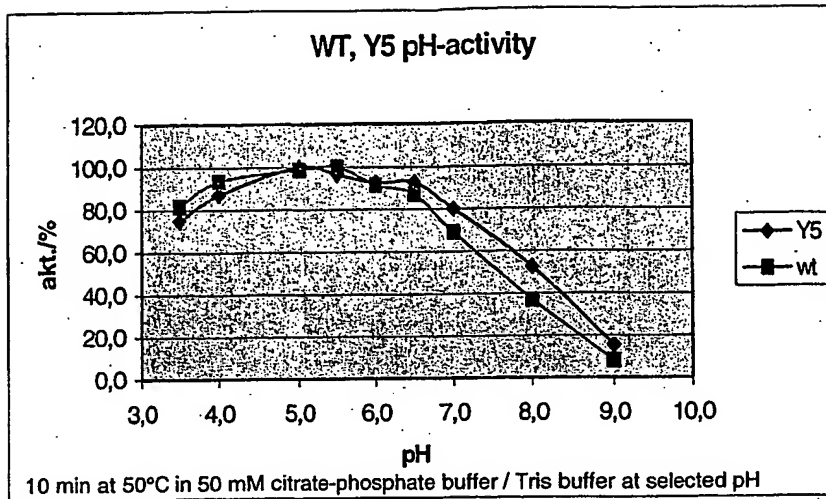


Figure 6

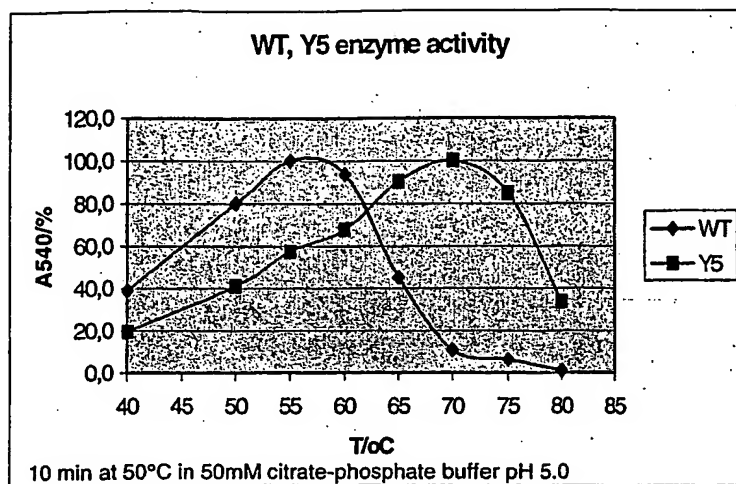


Figure 7

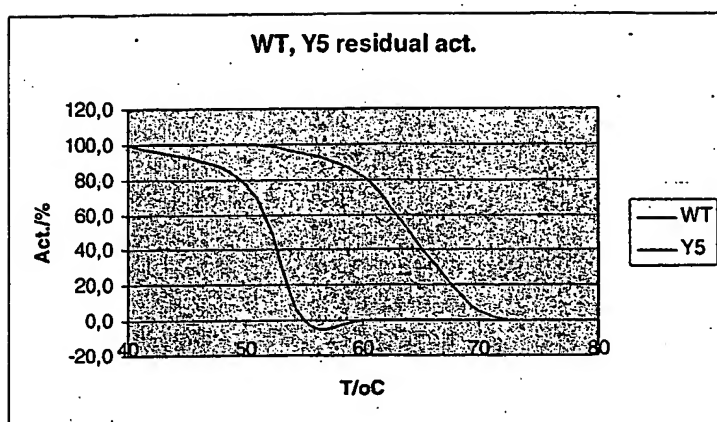


Figure 8

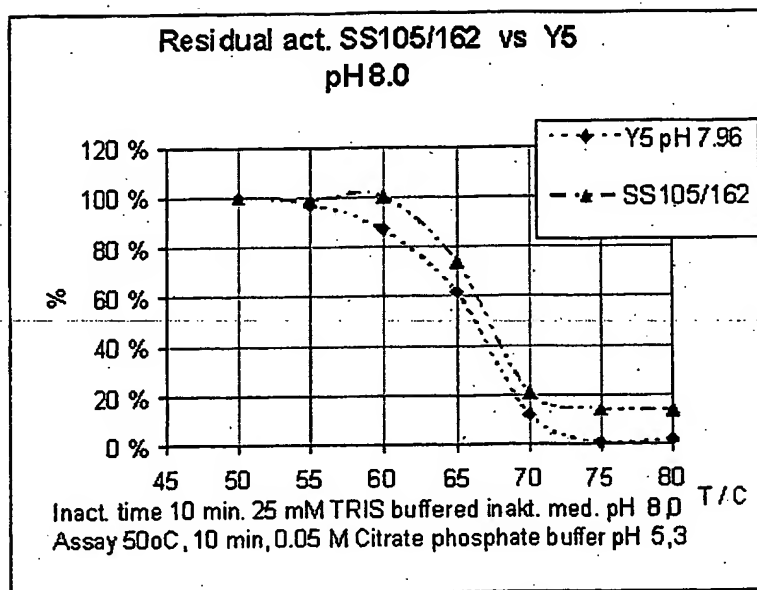


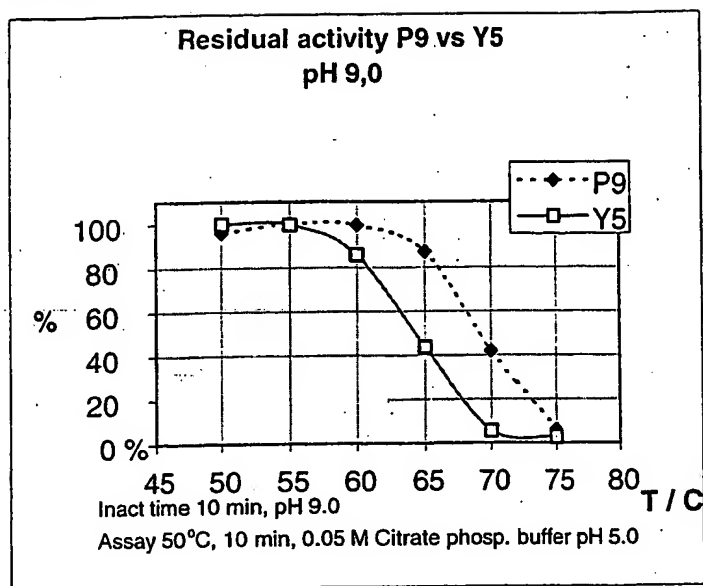
Figure 9.

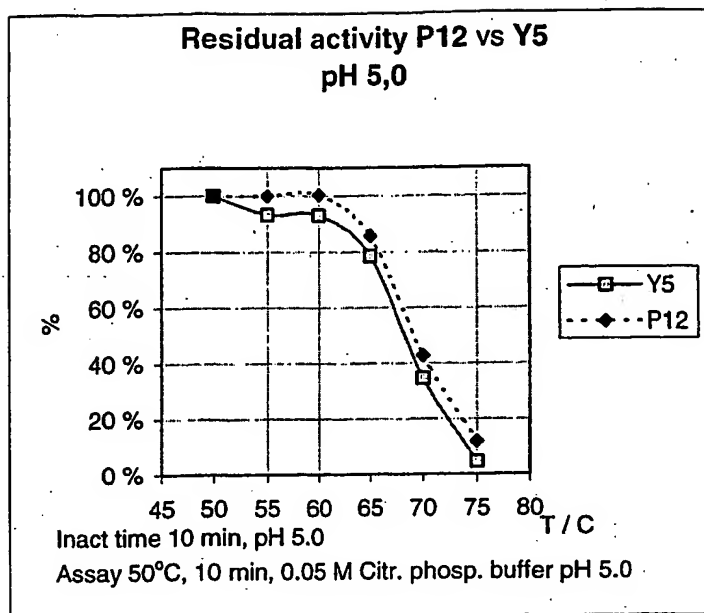
Figure 10.

Figure 11.

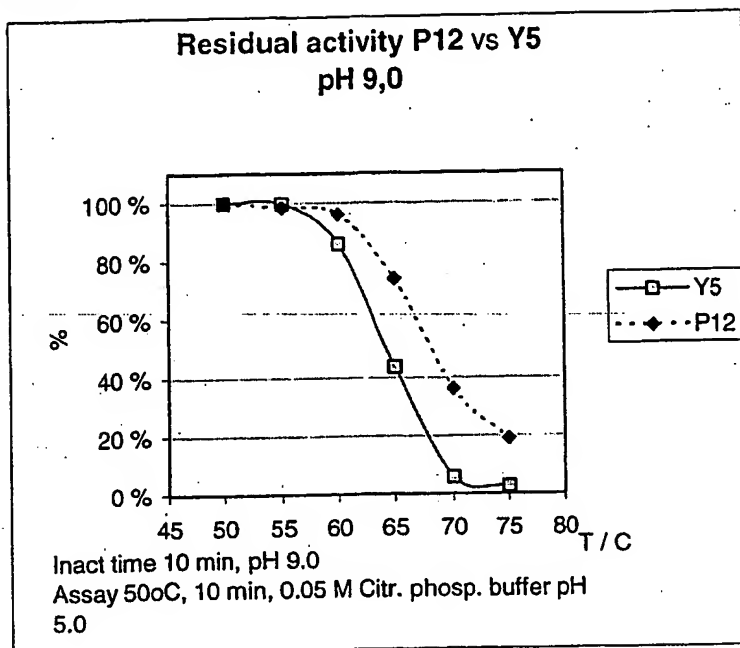


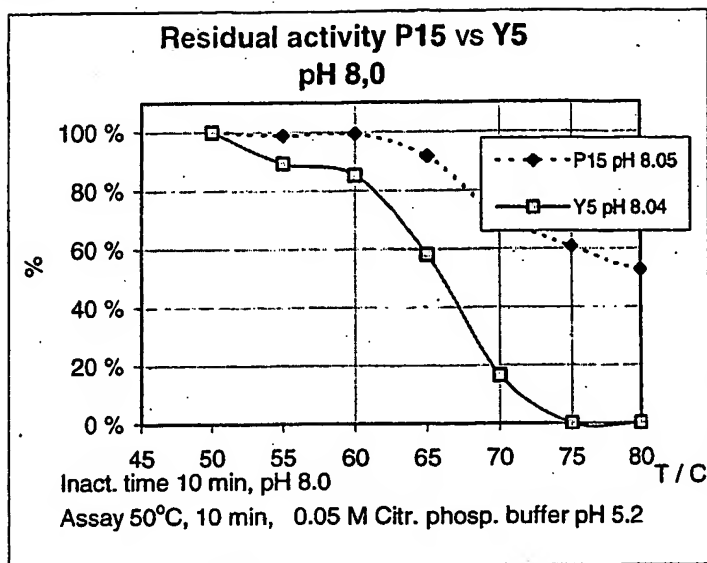
Figure 12.

Figure 13.

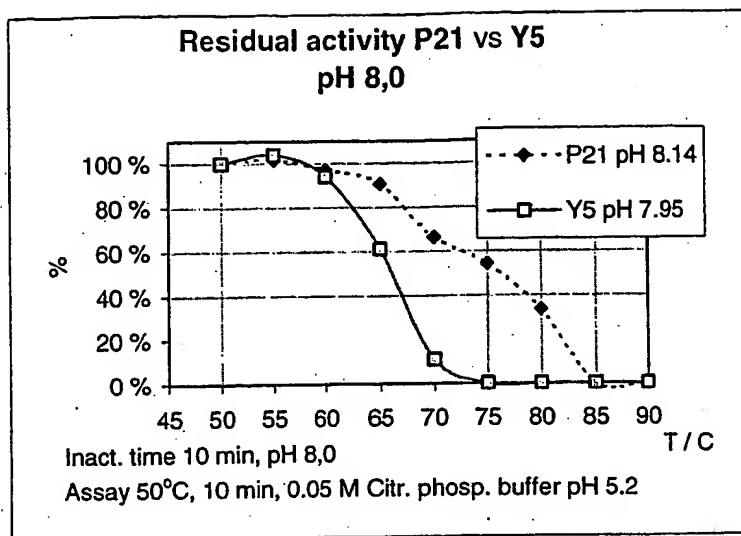


Figure 14.

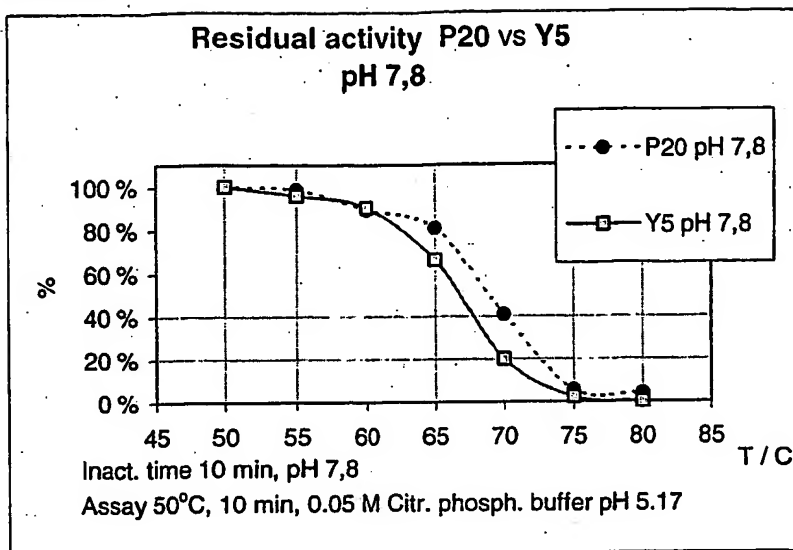


Figure 15.

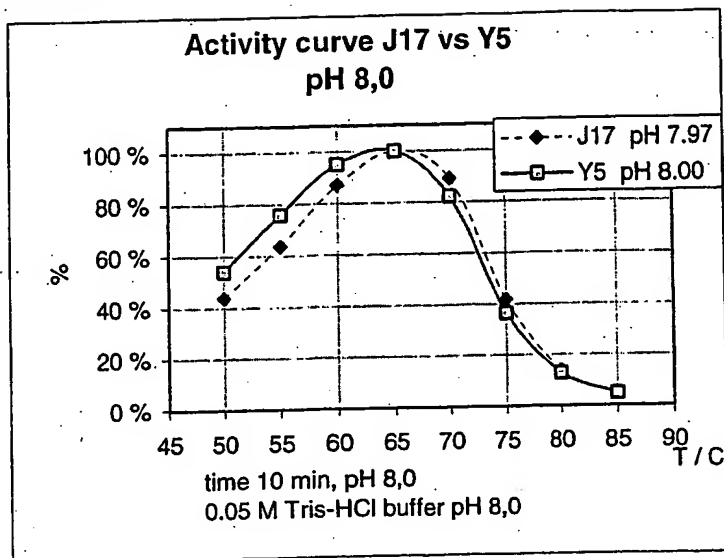


Figure 16.

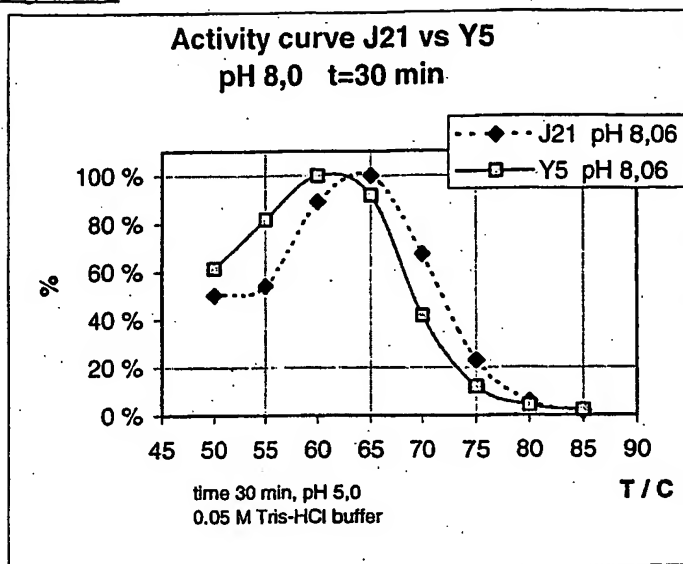


Figure 17

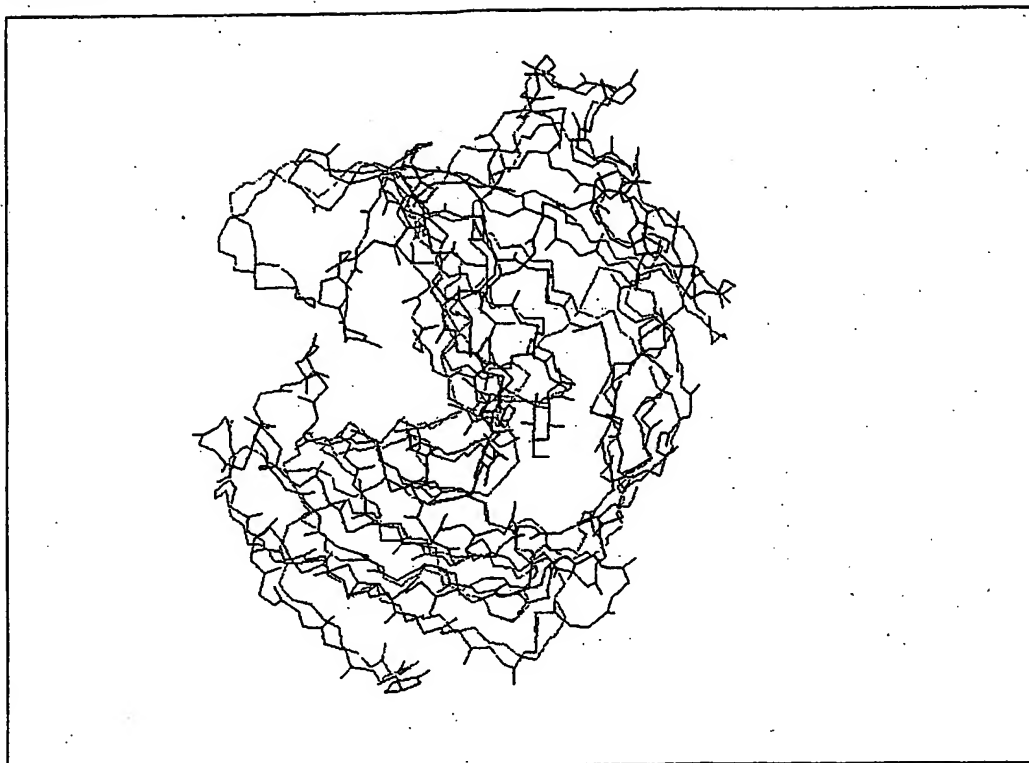


Figure 18

Trichoderma reesei Xyl II protein (high pl xylanase)
the full sequence, including signal and pro sequence

MVSFTSLLAGVAASGVLAAPAAEVESVAVEKRQTIQPGTGYNNGYFYSWNDHGHHGGVYTYNGPGGQFSVNWWSNSGNFVG
GKGWQPGTKNKNVINFSGSYNPNNGNSYLSVYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTS DGSVYDIYRTQRVNQPS
IIGTATFYQYWSVRRNRHSSGSVNTANHFNAWAQQGLTLGTM DYQIVAVEGYFSSGSASITVS (SEQ. ID NO: 1)

Trichoderma reesei XynII gene (high pl xylanase)
DNA from start codon to stop codon (includes a single intron)

ATGGTCTCCTTCACCTCCCTCCTCGCCGGCGTGC GCCGCCATCTCGGGCGTCTTGGCCGCTCCCGCCGCGGAGGTGGAATC
CGTGGCTGTGGAGAGCGCCAGACGATT CAGCCCGGCACGGGCTACAACAACGGCTACTTCTACTCGTACTGGAACGATG
GCCACGGCGCGTGACGTACACCAATGGTCCCGGGCGAGTTCTCCGTCAACTGGTCCAACCTCGGGCAACTTTGTGCGGC
GGCAAGGGATGGCAGCCCGGCACCAAGAACAAAGTAAGACTACCTACTCTTACCCCTTTGACCAACACAGCACACAACAA
TACAACACATGTGACTACCAATCATGGAATCGGATCTAACAGCTGTGTTTTCAAAAAAAGGGTCATCAACTTCTCGGGC
AGCTACAAACCCCAACGCAACAGCTACCTCTCCGTGTACGGCTGGTCCCGCAACCCCTGATCGAGTACTACATCGTCTCGA
GAACCTTTGGCACCTACAACCCCGTCCACGGCGCCACCAAGCTGGCGAGGTACCTCCGACGGCAGCGTCTACGACATTT
ACCGCACGCGCGGTCAACACGCGTCCATCATCGGACCGCCACCTTTTACCAGTACTGGTCCGTCGCCGCAACCCAC
CGCTCGAGCGGCTCCGTCAACACGCGGAACCACTTCAACGCGTGGGCTCAGCAAGGCTGACGCTCGGGACGATGGATT
CCAGATTGTGCCGTGGAGGGTACTTTAGCTCTGGCTCTGCTTCCATCACCGTCAGCTAA (SEQ. ID NO: 2)

Figure 19

Trichoderma reesei EGL III protein (endoglucanase III)
the full sequence, including signal sequence

MKFLQVLPAIPAALAQTSQDQWATFTGNGYTVSNLWLGASAGSGFGCVTAVSLSGGASWHADWQWSGGQNNVKSQNSQ
IAIPQKRTVNSISSMPTTASWSYSGSNIRANVAYDLFTAANPNHVITYSGDYELMIWLKYGDIGPIGSSQGTNVNNGQSW
TLYYGYNGAMQVYSFVAQTNTTNSGDVKNFFNYLRDNKGYNAAGQVLSYQFGTEPFTGSGTLNVASWTASIN
(SEQ. ID NO: 3)

Trichoderma reesei EG III gene (endoglucanase III)
DNA from start codon to stop codon (includes two introns)

ATGAAGTTCCTTCAAGTCCTCCCTGCCCTCATACCGGCCGCCCTGGCCAAACCAGCTGTGACCAGTGGGCAACCTTCAC
TGGCAACGGGTACACAGTCAGCAACAACCTTTGGGAGCATCAGCGGCTCTGGATTGGCTGCGTGACGGCGGTATCGC
TCAGCGCGGGCCCTCCTGGCACGCAGACTGGCAGTGGTCCGGCGGCCAGAACACGTCAAGTCGTACCGAACTCTCAG
ATTGCCATTCCCAGAAAGAGACCGTCAACAGCATCAGCAGCATGCCACCACTGCCAGCTGGAGCTACAGCGGGAGCAA
CATCCGCGCTAATGTTGCGTATGACTTGTACCCGAGCCCAACCGAATCATGTACGTACTCGGGAGACTACGAACTCA
TGATCTGGTAAGCCATAAGAAGTGACCCCTCCTTGATAGTTTCGACTAACACATGCTTGAGGCTTGGCAAATACGGCGA
TATTGGGCCGATTGGGTCTCACAGGGAACAGTCAACGTCGGTGGCCAGAGCTGGACGCTCTACTATGGCTACAACGGAG
CCATGCAAGTCTATTCTTTGTGGCCAGACCAACTACAGCGGAGATGTCAAGAACTTCTTCAATTATCTC
CGAGACAATAAAGGATACAACGCTGCAGGCCAATATGTTCTTAGTAAGTCAACCTCACTGTGACTGGGCTGAGTTTGTG
CAACGTTTGCTAACAAACCTTCGTATAGGCTACCAATTTGGTACCGAGCCCTTCACGGGCGAGTGGAACTCTGAACGTCG
CATCCTGGACCGCATCTATCAACTAA (SEQ. ID NO: 4)

Figure 20

atgggtgcctttccagccctcatctggcgtctaccagcattgccagttactctggcgtgacccacaggccctgagcctgagagcagtgtaacgtcacagagcgtggcaltgactgtgttctt
 ggagctcaaatgatcatcgcctgtgtgtagcatcaactacgaccaaaactaccaaaactggcggacaagtcagctattcgccttccaacacgtggcttctcagtgaaactgggaacactcaagatg
 actttgttgggcgttggtagcagactggatcttgcgttagggaggaactccctcatcattctgcactttgaagcattcttgaccaaaagcttcttagtcccaactttggcggctcttttagtg
 tcaacagcgggaactggcctgttccgtctatggctggagcaccaccccactgttgtagtactacatcatggaggacaacacacactaccacagaggtaccgtcaagggaaccgtcaccc
 agcgacggaggccacttaccatctgggagaatacccgtgtcaacgagccttccatocaggggcacagcgaccttaaccaggtacattcgtcgggaactcgtccacagggaccagcgggaactg
 ttactgtgcagaaccacttcaatgcttgggcctcgttggcctgcaccttgggcagatgaactaccaggttgcgtgtcgaaggctgggggtgtagtggttctgcctcacagagtgtagcagcaac
 tag

Xylanase I Amino Acid sequence

MVAFSSLICALTSTLAMPTGLEPESSVNVTERGMYDFVLGAHNDHRRRASINYDQNYQTGGQVSYSPTSNTGFSVNW
 N
 TQDDFVVGWTTGSSA.EDSSSFCTLKASSDQKLLVPSTLAALLVSTAELACFPSMAGAPTHWLSTTSWRITTTTQHR
 VPSREPSATEPLTPSGRIPVSTSLPSRAQRPSTSTFPCTGTRPGPAELLCRTTSMGLPRLACTLGR.TTRLSLSKAGVV
 VVLPHRVVSAT